Package ‘Interact’

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Type Package

Title Tests for marginal interactions in a 2 class response model

Version 1.1

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Description This package searches for marginal interactions in a binary response model. Interact uses permutation methods to estimate false discovery rates for these marginal interactions and has some, limited visualization capabilities

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NeedsCompilation yes

R topics documented:

`Interact-package` *Test marginal interactions for a model with binary response*

Description

This package tests all potential marginal interactions in a binary response model, and estimates false discovery rates at each potential cutoff.

Details

Package:	Interact
Type:	Package
Version:	1.0
Date:	2012-06-29
License:	GPL-2

Very straightforward to use. Accepts data in the form `X,y` and tests all marginal interactions. Only 2 functions: `interact` `plot.interact`

Author(s)

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References

Simon, N. and Tibshirani, R. (2012) *A Permutation Approach to Testing Marginal Interactions in Many Dimensions*, `http://www-stat.stanford.edu/~nsimon/TMIcor.pdf`

`interact` *Test marginal interactions for a model with binary response*

Description

Tests all potential marginal interactions, and estimates false discovery rates at each potential cutoff

Usage

```
interact(x, y, z = NULL, numPerm = 100, numFDR = 1000, method = "Pearson", verbose = TRUE)
```

Arguments

`x`	An n-by-p matrix of covariates - observations in rows, features in columns.
`y`	An n-vector of class labels taking on two values (eg 0,1 or A,B)
`z`	An optional secondary n-by-q matrix of covariates - observations in rows, features in columns.
`numPerm`	The number of permutations to run
`numFDR`	The number of marginal interactions you would like to estimate FDR for — default is 1000 (more interactions can increase runtime).
`method`	A string, either "Pearson" or "Spearman", indicating which type of correlation is to be used.
`verbose`	A boolean flag indicating whether current permutation number should be output.

Details

A correlation matrix is constructed for each class (according to method). The function then apply a fisher transformation to these values and takes their difference. These values are ordered, and permutations are used to assess false discovery rate estimates. If no Z matrix is included then all pairwise correlations are considered for variables in X. If a Z matrix is included then only correlations between X and Z variables are considered.

Value

`interaction.ordered`	A dataframe of the `numFDR` most significant marginal interactions (ordered from most significant to least significant). The first two columns indication the interaction and the third column gives an estimated q-value (False Discovery Rate).
`internals`	Variables used interally for methods relating to interact

Author(s)

Noah Simon, and Robert Tibshirani

References

Simon, N. and Tibshirani, R. (2012) *A Permutation Approach to Testing Marginal Interactions in Many Dimensions*, http://www-stat.stanford.edu/~nsimon/TMIcor.pdf

See Also

`plot`, `print`

Examples

```
set.seed(5)

n <- 100
p <- 10
s <- 5

X1 <- cbind(matrix(rnorm(n*s), ncol = s) + rnorm(n), matrix(rnorm(n*(p-s)), ncol = (p-s)))
X2 <- matrix(rnorm(n * p), ncol = p)

X <- rbind(X1, X2)

colnames(X) <- c("a","b","c","d","e","f","g","h","i","j")
y <- c(rep("y",n),rep("n",n))

fit <- interact(X,y)
print(fit)
plot(fit)

## Bigger Example (restricting the number of top interactions to consider)
## Not run:
## Not run:
```

```
n <- 300
p <- 500
s <- 10

X1 <- cbind(matrix(rnorm(n*s), ncol = s) + rnorm(n), matrix(rnorm(n*(p-s)), ncol = (p-s)))
X2 <- matrix(rnorm(n * p), ncol = p)
X <- rbind(X1, X2)

y <- c(rep("y",n),rep("n",n))

fit <- interact(X,y, numFDR = 50)
## Restricts the number of most significant interactions to consider to 50
print(fit)
plot(fit)

## End(Not run)

## Example Comparing (simulated) Genes and Enviromental Variables

## Not run:
n <- 100
p1 <- 100
p2 <- 10


Genes <- matrix(rnorm(n * p1), ncol = p1)
Environment <- matrix(rnorm(n * p2), ncol = p2)

y <- c(rep("y",n/2),rep("n",n/2))

fit <- interact(X = Genes,y, Z = Environment, numFDR = 50)
## Restricts the number of most significant interactions to consider to 50
print(fit)
plot(fit)

## End(Not run)
## End(**Not run**)
```

`plot.interact` *Plots FDR estimates for interact object*

Description

This plots an estimated FDR curve for an object output by the function `interact`

Usage

```
## S3 method for class 'interact'
plot(x, numInteractions = nrow(x$interaction.ordered), ...)
```

Arguments

`x`	A variable of class `interact` — the output of function `interact`
`numInteractions`	The number of most significant interactions one would like plotted
`...`	Other arguments which the user would like to pass to the general `plot` function

Author(s)

Noah Simon, and Robert Tibshirani

References

Simon, N. and Tibshirani, R. (2012) *A Permutation Approach to Testing Marginal Interactions in Many Dimensions*, http://www-stat.stanford.edu/~nsimon/TMIcor.pdf

See Also

`interact`, `print`

`print.interact` *Prints Basic output for interaction object*

Description

This prints the function call and first 10 significant interactions for an object output by the function `interact`

Usage

```
## S3 method for class 'interact'
print(x, ...)
```

Arguments

`x`	A variable of class `interact` — the output of function `interact`
`...`	Other arguments which the user would like to pass to the general `print` function

Author(s)

Noah Simon, and Robert Tibshirani

References

Simon, N. and Tibshirani, R. (2012) *A Permutation Approach to Testing Marginal Interactions in Many Dimensions*, http://www-stat.stanford.edu/~nsimon/TMIcor.pdf

See Also

`interact`, `plot`

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